# WEST Search History

DATE: Wednesday, June 25, 2003

| Set Name side by side | Query | Hit Count | Set Name result set |
|---|---|---|---|
| | *DB=USPT,PGPB,JPAB,EPAB,DWPI; PLUR=YES; OP=OR* | | |
| L6 | L5 and gene with delet$ with (syncytial or RSV) | 48 | L6 |
| L5 | l1 not l2 | 132 | L5 |
| L4 | L3 and syncytial | 2 | L4 |
| L3 | l2 and (respiratroy or RSV) same (gene with deletion) | 15 | L3 |
| L2 | L1 and @ad<19960715 | 32 | L2 |
| L1 | (RSV or respiratory adj syncytial) same (gene with delet$4) | 164 | L1 |

END OF SEARCH HISTORY

STN Search History

FILE 'HOME' ENTERED AT 08:02:29 ON 25 JUN 2003

L1 209 (RESPIRATORY (A) SYNCYTIAL OR RSV) AND ((MAJOR (3A) NUCLEOCAPSID OR N) (P) (NUCELOCAPSID (3N) PHOSPHOPROTEIN OR P) (P) (LARGE ADJ POLYMERASE OR L))

L3 1 L2 AND (DELETION OR MUTATION OR TRUNCATION) (S) (SMALL (A) HYRDO PHOBIC OR SH) (A) (GENE OR PROTEIN)

FILE 'MEDLINE, CAPLUS, BIOSIS, EMBASE, SCISEARCH' ENTERED AT 08:03:04 ON 25 JUN 2003

L1 209 S (RESPIRATORY (A) SYNCYTIAL OR RSV) AND ((MAJOR (3A) NUCLEOCAP
L2 74 DUP REM L1 (135 DUPLICATES REMOVED)
L3 1 S L2 AND (DELETION OR MUTATION OR TRUNCATION) (S) (SMALL (A) HY
L4 23 S L2 NOT PY>1996
L5 0 S L4 AND (POLYMERASE (2A) ELONGATION)
L6 4 S L4 AND (M2 OR M2##### OR M2-1 OR M2 (A) ORF1 OR M2-ORF1)
L7 6 S L2 AND ELONGATION (S) (FACTOR OR PROTEIN )
L8 2 S L7 AND L4
L9 0 S L8 NOT L6

L6 ANSWER 1 OF 4 MEDLINE
AN 96133881 MEDLINE
DN 96133881 PubMed ID: 8552680
TI Transcription elongation factor of **respiratory syncytial** virus, a nonsegmented negative-strand RNA virus.
AU Collins P L; Hill M G; Cristina J; Grosfeld H
CS Laboratory of Infectious Diseases, National Institute of Allergy and Infectious Diseases, National Institutes of Health, Bethesda, MD 20892-0720, USA.
SO PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (1996 Jan 9) 93 (1) 81-5.
Journal code: 7505876. ISSN: 0027-8424.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199602
ED Entered STN: 19960306
Last Updated on STN: 19960306
Entered Medline: 19960222
AB RNA synthesis by the paramyxovirus **respiratory syncytial** virus, a ubiquitous human pathogen, was found to be more complex than previously appreciated for the nonsegmented negative-strand RNA viruses. Intracellular RNA replication of a plasmid-encoded "minigenome" analog of viral genomic RNA was directed by coexpression of the **N**, **P**, and **L** proteins. But, under these conditions, the greater part of mRNA synthesis terminated prematurely. This difference in processivity between the replicase and the transcriptase was unanticipated because the two enzymes ostensively shared the same protein subunits and template. Coexpression of the **M2** gene at a low level of input plasmid resulted in the efficient production of full-length mRNA and, in the case of a dicistronic minigenome, sequential transcription. At a higher level, coexpression of the **M2** gene inhibited transcription and RNA replication. The **M2** mRNA contains two overlapping translational open reading frames (ORFs), which were segregated for further analysis. Expression of the upstream ORF1, which encoded the previously described 22-kDa **M2** protein, was associated with transcription elongation. A model involving this protein in the balance between transcription and replication is proposed. ORF2, which lacks an assigned protein, was associated with inhibition of RNA synthesis. We propose that this activity renders nucleocapsids synthetically quiescent prior to incorporation into virions.

L6 ANSWER 2 OF 4 MEDLINE
AN 96102154 MEDLINE
DN 96102154 PubMed ID: 8524804
TI Production of infectious human **respiratory syncytial** virus from cloned cDNA confirms an essential role for the transcription elongation factor from the 5' proximal open reading frame of the **M2** mRNA in gene expression and provides a capability for vaccine development.
AU Collins P L; Hill M G; Camargo E; Grosfeld H; Chanock R M; Murphy B R
CS Laboratory of Infectious Diseases, National Institute of Allergy and Infectious Diseases, Bethesda, MD 20892-0720, USA.
SO PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (1995 Dec 5) 92 (25) 11563-7.
Journal code: 7505876. ISSN: 0027-8424.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English

FS Priority Journals
EM 199601
ED Entered STN: 19960219
Last Updated on STN: 19960219
Entered Medline: 19960124
AB Infectious human **respiratory syncytial** virus (**RSV**) was produced by the intracellular coexpression of five plasmid-borne cDNAs. One cDNA encoded a complete positive-sense version of the **RSV** genome (corresponding to the replicative intermediate RNA or antigenome), and each of the other four encoded a separate **RSV** protein, namely, the **major nucleocapsid N** protein, the **nucleocapsid P** phosphoprotein, the **major** polymerase **L** protein, or the protein from the 5' proximal open reading frame of the **M2** mRNA [**M2**(**ORF1**)]. **RSV** was not produced if any of the five plasmids was omitted. The requirement for the **M2**(**ORF1**) protein is consistent with its recent identification as a transcription elongation factor and confirms its importance for **RSV** gene expression. It should thus be possible to introduce defined changes into infectious **RSV**. This should be useful for basic studies of **RSV** molecular biology and pathogenesis; in addition, there are immediate applications to the development of live attenuated vaccine strains bearing predetermined defined attenuating mutations.

L6 ANSWER 3 OF 4 MEDLINE
AN 92327836 MEDLINE
DN 92327836 PubMed ID: 1626423
TI Gene junction sequences of bovine **respiratory syncytial** virus.
AU Zamora M; Samal S K
CS Regional College of Veterinary Medicine, University of Maryland, College Park 20742.
SO VIRUS RESEARCH, (1992 Jun) 24 (1) 115-21.
Journal code: 8410979. ISSN: 0168-1702.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199208
ED Entered STN: 19920821
Last Updated on STN: 19920821
Entered Medline: 19920813
AB The nucleotide sequences of seven gene junctions (**N-P**, **P**-M, M-SH, SH-G, G-F, F-**M2** and **M2-L**) of bovine **respiratory syncytial** virus (BRSV) strain A51908 were determined by dideoxynucleotide sequencing of cDNAs from polytranscript mRNAs and from genomic RNA. By comparison with the consensus sequences derived from human **respiratory syncytial** virus (HRSV) mRNAs, gene-start and gene-end sequences were found in all BRSV mRNAs. There was a perfect match between the BRSV and HRSV in all gene-start sequences, except for the sequence of the SH gene which contained one nucleotide difference compared to HRSV A2; and the gene-start sequence of the **L** gene, which was one nucleotide shorter than the corresponding sequence of HRSV. Analysis of the intergenic regions showed a high degree of divergence in the nucleotide sequence between BRSV and HRSV. However, the length of the nucleotides in the intergenic sequences was similar for a given gene junction. As in the case of HRSV, the **M2** and **L** genes of BRSV overlap by 68 nucleotides, suggesting a similar transcription attenuation mechanism. The sequences of the overlap, corresponding to the 3' end of the **L** gene, were almost identical between BRSV and HRSV.

L6 ANSWER 4 OF 4 SCISEARCH COPYRIGHT 2003 THOMSON ISI
AN 95:716951 SCISEARCH
GA The Genuine Article (R) Number: RZ285
TI THE COMPLETE GENOME STRUCTURE AND PHYLOGENETIC RELATIONSHIP OF INFECTIOUS HEMATOPOIETIC NECROSIS VIRUS
AU MORZUNOV S P; WINTON J R; NICHOL S T (Reprint)
CS CTR DIS CONTROL & PREVENT, DIV VIRAL & RICKETTSIAL DIS, 1600 CLIFTON RD NE, ATLANTA, GA, 30333 (Reprint); UNIV NEVADA, DEPT BIOCHEM, RENO, NV, 89557; UNIV NEVADA, DEPT MICROBIOL, RENO, NV, 89557; NW BIOL SCI CTR, NATL BIOL SERV, SEATTLE, WA, 98115
CYA USA
SO VIRUS RESEARCH, (OCT 1995) Vol. 38, No. 2-3, pp. 175-192.
ISSN: 0168-1702.
DT Article; Journal
FS LIFE
LA ENGLISH
REC Reference Count: 64
*ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS*

AB Infectious hematopoietic necrosis virus (IHNV), a member of the family Rhabdoviridae, causes a severe disease with high mortality in salmonid fish. The nucleotide sequence (11,131 bases) of the entire genome was determined for the pathogenic WRAC strain of IHNV from southern Idaho. This allowed detailed analysis of all 6 genes, the deduced amino acid sequences of their encoded proteins, and important control motifs including leader, trailer and gene junction regions. Sequence analysis revealed that the 6 virus genes are located along the genome in the 3' to 5' order: nucleocapsid (**N**), polymerase-associated phosphoprotein (**P** or M1), matrix protein (M or **M2**), surface glycoprotein (G), a unique non-virion protein (NV) and virus polymerase ( **L**). The IHNV genome RNA was found to have highly complementary termini (15 of 16 nucleotides). The gene junction regions display the highly conserved sequence UCURUC(U)(7)RCCGUG(**N**)(4)CACR (in the vRNA sense), which includes the typical rhabdovirus transcription termination/polyadenylation signal and a novel putative transcription initiation signal. Phylogenetic analysis of M, G and **L** protein sequences allowed insights into the evolutionary and taxonomic relationship of rhabdoviruses of fish relative to those of insects or mammals, and a broader sense of the relationship of non-segmented negative-strand RNA viruses. Based on these data, a new genus, piscivirus, is proposed which will initially contain IHNV, viral hemorrhagic septicemia virus and Hirame rhabdovirus.